

PF 30-APR-2001; 2001WO-DK000293.  
 XX 28-APR-2000; 2000DK-00000707.  
 PR 10-MAY-2000; 2000US-0203345P.  
 PR 28-FEB-2001; 2001DK-00000327.  
 PR 21-MAR-2001; 2001US-0277817P.  
 XX

XX (NOVO ) NOVOZYMES AS.  
 XX

XX Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;  
 XX

XX WPI; 2001-626552/72.  
 XX

XX Selecting protein variants having modified immunogenicity, used to  
 PT produce vaccines, detergents and personal care compositions, involves  
 PT localizing epitope sequences on the three-dimensional structure of a  
 PT protein.  
 XX

XX Claim 99; Page 510-512; 513pp; English.  
 XX

XX The invention relates to selecting a protein variant having modified  
 CC immunogenicity, compared to a parent protein, comprising using the  
 CC antibody binding sequence to localise epitope sequences on the three  
 CC dimensional structure of the parent protein and defining an epitope area  
 CC including amino acids within 5 Angstrom of the epitope amino acids. The  
 CC method is useful for identifying structural epitopes on the 3-dimensional  
 CC surface of commercial and environmental allergens. Compositions  
 CC containing the protein variants are used as vaccines, detergents and  
 CC personal care compositions, e.g. shampoo, balsam, hair conditioners, hair  
 CC waving compositions, hair dyeing compositions, hair tonic, hair liquid,  
 CC hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,  
 CC shaving foam, cream soap, skin milk or foundation. The present sequence  
 CC is that of a polypeptide of the invention  
 XX

XX Sequence 471 AA;  
 SQ

Query Match 92.7%; Score 1440; DB 4; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPDTFTWTRDGLVL 84

DB 1 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPDTFTWTRDGLVL 60

QY 85 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGWS 144

DB 61 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGWS 120

QY 145 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQGYDLWEE 204

DB 121 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQGYDLWEE 180

QY 205 VNGSFFFTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 264

DB 181 VNGSFFFTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 240

QY 265 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 295

DB 241 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 271

RESULT 12

AAW55979

ID AAW55979

XX AAW55979;

XX 27-JUL-1998 (first entry)

XX Aspergillus awamori glucoamylase mutant S411A.

XX Aspergillus awamori; glucoamylase; Aspergillus sp; mutant; fungal; food;  
 XX fructose; corn; sweetener; 1,4-alpha-D-glucan glucohydrolase;

KW genetic engineering.  
 XX

OS Synthetic.  
 OS

OS Aspergillus awamori.  
 OS

PN WO9803639-A1.  
 XX

XX 29-JAN-1998.  
 XX

XX 24-JUL-1997; 97WO-US012983.  
 PF

XX 24-JUL-1996; 96US-0022578P.  
 PR

XX 02-AUG-1996; 96US-0023077P.  
 PR

XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 PA

XX Allen M, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R;  
 PI Ford C;  
 PI

XX WPI; 1998-120764/11.  
 DR

XX Genetically engineered fungal glucoamylase - useful in, e.g. food  
 PT industry for production of high fructose corn sweeteners.  
 PT

XX Claim 10; Page; 97pp; English.  
 PS

XX The present sequence represents a specifically claimed mutant  
 CC glucoamylase from Aspergillus awamori (1,4-alpha-D-glucan  
 CC glucosylase). The present invention describes fungal glucoamylases  
 CC (FG) comprising: a mutation pair Asn20Cys coupled with Ala27Cys forming a  
 CC disulphide bond between the 2 members of the pair; and a 311-314Loop or  
 CC Ser411Ala mutation. FG can be used in industry for the production of high  
 CC fructose corn sweeteners, while the glucose produced by glucoamylase can  
 CC be crystallised or used in fermentation to produce organic products, e.g.  
 CC citric acid, ascorbic acid, lysine, glutamic acid or ethanol for  
 CC beverages and fuel. The mutations provide increased thermal stability,  
 CC reduced isomaltose formation and increased pH optimum. N.B. The present  
 CC sequence is not given in the specification but is derived from SEQ ID  
 CC NO:1 as stated in the claim  
 XX

XX Sequence 616 AA;  
 SQ

Query Match 92.7%; Score 1440; DB 2; Length 616;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPDTFTWTRDGLVL 84

DB 1 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPDTFTWTRDGLVL 60

QY 85 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGWS 144

DB 61 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGWS 120

QY 145 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQGYDLWEE 204

DB 121 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQGYDLWEE 180

QY 205 VNGSFFFTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 264

DB 181 VNGSFFFTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 240

QY 265 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 295

DB 241 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 271

RESULT 13

AAI515176

ID AAI515176 standard; protein; 616 AA.

XX AAI515176;

XX